SHORT COMMUNICATION

Comprehensive linkage map of bovine chromosome 11

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Summary

The results of genotypic data contributed to the International Society of Animal Genetics (ISAG) Bovine Chromosome 11 (BTA11) Workshop are presented. Six laboratories contributed a total of 26 199 informative meioses from 80 loci. Thirty-six loci were typed by at least two independent laboratories and were used to construct a consensus linkage map of the chromosome. The remaining loci were subsequently incorporated into a comprehensive map. The sex-averaged consensus map covered 128.9 cM. The female consensus map was 101.2 cM, while the male consensus map was 129.8 cM. The comprehensive sex-averaged map was 134.2 cM and the average genetic distance between loci was 1.72 cM.

Keywords bovine, BTA11, comprehensive map, consensus map, linkage map.

The International Society for Animal Genetics (ISAG) has promoted the construction of chromosomal comprehensive linkage maps integrating data from several populations. To date, there are several chromosomes already published from this effort (Beever *et al.* 1996; Taylor *et al.* 1998; Casas *et al.* 1999; Gu *et al.* 2000). The objective of the present report was to construct a comprehensive map of bovine chromosome 11 including information from all genetic markers available.

Genotypic information from six bovine pedigrees were submitted to the organizing laboratory at the U.S. Meat Animal Research Center, Clay Center, Nebraska. All data were submitted in a standardized format for analysis by CRIMAP V. 2.4 (Green *et al.* 1990). A total of 80 loci were represented in the combined data. Genotypic data from the U.S. Meat Animal Research Center (Kappes *et al.* 1997), Norwegian Cattle Map (Våge *et al.* 2000), Illinois Reference/Resource Families (Ma *et al.* 1996), Munich Veterinary University ADR Genome Project (Thomsen *et al.* 2000), Adelaide-Ag Research Cattle QTL mapping project (Morris *et al.* 2000), and the Canadian Beef Cattle Reference Herd (http://skyway.usask.ca/~schmutz/) were submitted. The number of marker loci submitted by each laboratory was 73, 13, 14, 13, 16 and 8, respectively. Each dataset was analysed independently using the TWOPOINT, FLIPS and CHROMPIC options of CRIMAP (Green *et al.* 1990). The CHROMPIC option was used to identify double-crossovers and to detect potential genotyping errors. Double-crossovers were ignored given the impossibility of rerunning a marker in any given dataset.

Genotypic data were merged into a single dataset using the MERGE option of CRIMAP. Thirty-six markers typed by more than one laboratory were used to produce the consensus map. FLIPS3 was implemented to test for revisions in marker order after including all markers. These loci were used to generate sex-averaged (128.9 cM), female (101.2 cM) and male (129.8 cM) consensus maps of BTA11 (data not shown).

Eighty loci were included in the analysis to produce the comprehensive map of BTA11 (Fig. 1). Markers from the consensus map (bolded in Fig. 1) served as the framework

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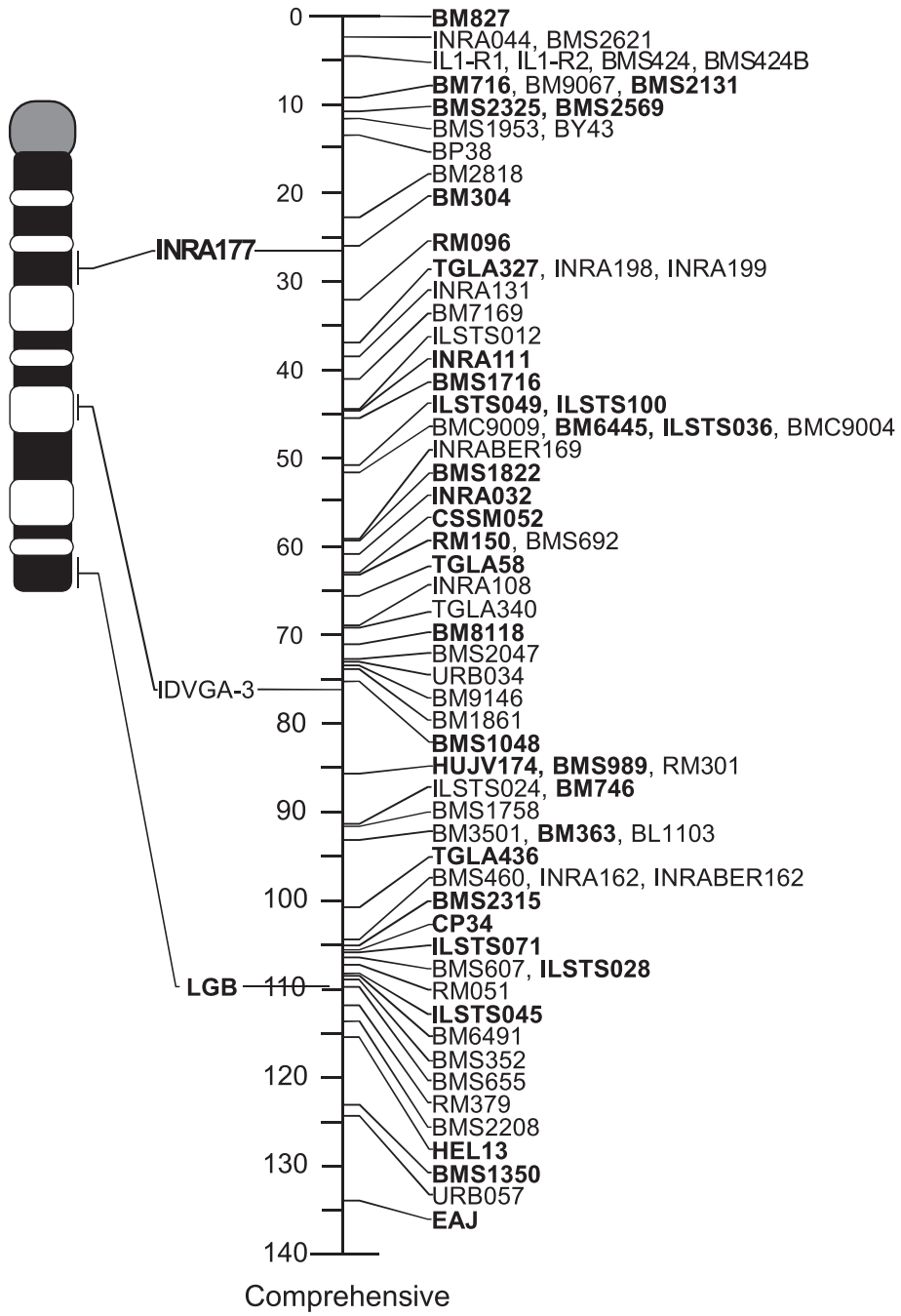

Figure 1 Sex-averaged comprehensive map of BTA11 developed from all markers submitted by participating laboratories. Markers in bold were used to generate the consensus map.

for including the remaining markers. The length of the sex-averaged comprehensive map was 134.2 cM, while the female and male maps were 106.6 and 136.1 cM, respectively (data not shown). The average interval was 1.72 cM and only the interval between BP38 and BM2818 was equal to 10 cM.

Chromosome coverage of BTA11 has been expanded beyond previously published maps (Kappes *et al.* 1997). Markers URB057 and EAJ were incorporated 0.6 and 9.7 cM distal to BMS1350, extending the telomeric coverage of the chromosome by 10.3 cM. The comprehensive map provides more chromosomal coverage than any

individual map. Expansion of the male consensus and comprehensive maps was observed. A similar finding was found by Casas *et al.* (1999). Expansion could be attributed to genotyping double-crossovers in contributed data, or bias in the estimation of distances by CRIMAP.

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